

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
ATGCGCGGCT	CGCGGCTGG	CTGCTGGCG	CTGCTGCTAC	CGCTGCTGTC	GCTACTGTC	60
MetProProS	erGlyLeuAr	gLeuLeuPro	LeuLeuLeuP	roLeuLeuTr	pLeuLeuVal	
CTGAGCGCTG	GCGCGCGGCG	CGCGGACTA	TCCACCTGCA	AGACTATCGA	CATGGAGCTG	120
LeuThrProG	lyProProAl	aAlaGlyLeu	SerThrCysL	ysThrIleAs	pMetGluLeu	
GTGAAGCGGA	AGCGCATCGA	GGCCATCGCG	GGCCAGATCC	TGTCCAAGCT	GCGGCTCGCC	180
ValLysArgL	ysArgIleGl	uAlaIleArg	GlyGlnIleL	euSerLysLe	uArgLeuAla	
AGCGCGCGGA	GCGCGGCGGA	GGTGGCGGCG	GGCGCGGCTG	CGAGGCGCGT	GCTGCGCGCTG	240
SerProProS	erGlnGlyGl	uValProPro	GlyProLeuP	roGluAlaVa	lLeuAlaLeu	
TACAACAGCA	CGCGCGACCG	GGTGGCGGCG	GAGAGTGCAG	AACCGGAGCC	CGAGCGCTGAG	300
TyrAsnSerT	hrArgAspAr	gValAlaGly	GluSerAlaG	luProGluPr	oGluProGlu	
GCGGACTACT	ACGCCAAGGA	GGTCAACCGC	GTGCTAATGG	TGGAAACCCA	CAACGAAATC	360
AlaAspTyrT	yrAlaLysGl	uValThrArg	ValLeuMetV	alGluThrHi	sAsnGluIle	
TATGACAAGT	TCAAGCAGAG	TACACACAGC	ATATATATGT	TCTTCAACAC	ATCAGAGCTC	420
TyrAspLysP	heLysGlnSe	rThrHisSer	IleTyrMetP	hePheAsnTh	rSerGluLeu	
CGAGAAGCGG	TACCTGAACC	CGTGTTCGTC	TCCCGGCGAG	AGCTGCGTCT	GCTGAGGAGG	480
ArgGluAlaV	alProGluPr	oValLeuLeu	SerArgAlaG	luLeuArgLe	uLeuArgArg	
CTCAAGTTAA	AAGTGGAGCA	GCAAGTGGAG	CTGTACCAGA	AATACAGCAA	CAATTCCTGG	540
LeuLysLeuL	ysValGluGl	nHisValGlu	LeuTyrGlnL	ysTyrSerAs	nAsnSerTrp	
CGATACCTCA	GCAACCGGCT	GCTGGCAACC	AGCGACTCCG	CAGAGTGGTT	ATCTTTTGAT	600
ArgTyrLeuS	erAsnArgLe	uLeuAlaPro	SerAspSerP	roGluTrpLe	uSerPheAsp	
GTACCGGAG	TTGTGGCGCA	GTGGTTGAGC	CGTGGAGGGG	AAATTGAGGG	CTTTGGGCTT	660
ValThrGlyV	alValArgGl	nTrpLeuSer	ArgGlyGlyG	luIleGluGl	yPheArgLeu	
AGCGCGGACT	GCTCTGTGTA	CAGCAGGGAT	AACACACTGC	AAGTGGACAT	CAACGGGTTC	720
SerAlaHisC	ysSerCysAs	pSerArgAsp	AsnThrLeuG	InValAspIl	eAsnGlyPhe	
ACTACCGGCG	GCGGAGGTGA	CTGGGCCACC	ATTCAATGGCA	TGAACCGGCG	TTTCCTGCTT	780
ThrThrGlyA	rgArgGlyAs	pLeuAlaThr	IleHisGlyM	etAsnArgPr	oPheLeuLeu	
CTCATGGCCA	CGCGGCTGGA	GAGGGGCGAG	CATCTGCAAA	GCGAATTGCG	GGGAGGCGGA	840
LeuMetAlaT	hrProLeuGl	uArgAlaGln	HisLeuGlnS	enGluPheGl	yGlyGlyGly	
TTCCCGCTCG	GGCTTTGGGC	GGGAGGGGGC	TCAAGGGGCG	CAATCAACTA	TAAGCAGCTC	900
SerProLeuG	lyLeuTrpAl	aglyGlyGly	SerAlaAlaA	laIleAsnTy	rLysGlnLeu	
CAGCTCCAG	AAAGCAGGAA	CATTGGGAAA	TGTACAGGAG	TCTTGGAGCA	GCTGAATGGA	960
GlnLeuGlnG	luArgThrAs	nIleArgLys	CysGlnGluL	euLeuGluGl	nLeuAsnGly	

Fig. 1

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
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CAGAAGAGTT	ACACTGCCCTT	TGCCATOCOA	GAGATGCTOC	AGAATGICTT	TCTTGICTTC	1080
GlnLysSerT	yrThrAlaPh	eAlaIleGln	GluMetLeuG	InAsnValPh	eLeuValPhe	
AGAAACAATT	TCTCCAGCAC	TGGGTGGAAT	GAGACTATTG	TTGTACGTCT	CCTGGATGAA	1140
ArgAsnAsnP	heSerSerTh	rGlyTrpAsn	GluThrIleV	alValArgLe	uLeuAspGlu	
CTCCACCAGC	AGACAGTGT	TCTGAAGACA	GTACTAGAGC	AAAAGCAAGA	GGAAAGATTG	1200
LeuHisGlnG	InThrValPh	eLeuLysThr	ValLeuGluG	luLysGlnGl	uGluArgLeu	
AAGTGGGAGA	TGTCTCAAC	TGCTCTCCAC	TTGAAGAGCT	ATTACTGGAG	GGTGCAAAGG	1260
ThrTrpGluM	etSerSerTh	rAlaLeuHis	LeuLysSerT	yrTyrTrpAr	gValGlnArg	
TACCTTAAAC	TCATGAAGTA	CAACAGCTAC	GCTTCGATCG	TGGTCCGAGC	AGAGATCTTC	1320
TyrLeuLysL	euMetLysTy	rAsnSerTyr	AlaTrpMetV	alValArgAl	aGluIlePhe	
AGGAACTTTC	TCATCATTCG	AAGACTTACC	AGAAACTTCC	AAACTGATC	TAGACC	1376
ArgAsnPheL	euIleIleAr	gArgLeuThr	ArgAsnPheG	InAsn...Se	rArg	

[illegible]

ifn+MMP+TGFB Sequence

10	20	30	40	50	60	
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TCCATCAACT	ATAAGCAGCT	CCAGCTCCAA	GAAAGGACGA	ACATTGGGAA	ATGTCAGGAG	120
SerIleAsnT	yrLysGlnLe	uGlnLeuGln	GluArgThrA	snIleArgLy	sCysGlnGlu	
CTCCTGGAGC	AGCTGAATGG	AAAGATCAAC	CTCAGCTACA	GGGCGGACTT	CAAGATCCCT	180
LeuLeuGluG	InLeuAsnGl	yLysIleAsn	LeuThrTyrA	rgAlaAspPh	eLysIlePro	
ATGGAGATGA	CCGAGAAGAT	GCAGAAGAGT	TACACTGCCT	TTGCCATCCA	AGAGATGCTC	240
MetGluMetT	hrGluLysMe	tGlnLysSer	TyrThrAlaP	heAlaIleGl	nGluMetLeu	
CAGAATGTCT	TTCTGTCTCT	CAGAAACAAT	TTCTCCAGCA	CTGGGTGGAA	TGAGACTATT	300
GlnAsnValP	heLeuValPh	eArgAsnAsn	PheSerSerT	hrGlyTrpAs	nGluThrIle	
GTTGTACGTC	TCCTGGATGA	ACTCCACCAG	CAGACAGTGT	TTCTGAAGAC	AGTACTAGAG	360
ValValArgL	euLeuAspGl	uLeuHisGln	GlnThrValP	heLeuLysTh	rValLeuGlu	
GAAAAGCAAG	AGGAAAGATT	GACGTGGGAG	ATGTCTCTCA	CTGCTCTCCA	CTTGAAGAGC	420
GluLysGlnG	luGluArgLe	uThrTrpGlu	MetSerSerT	hrAlaLeuHi	sLeuLysSer	
TATTACTGGA	GGGTGCAAAG	GTACCTTAAA	CTCATGAAGT	ACAACAGCTA	CGCCTGGATG	480
TyrTyrTrpA	rgValGlnAr	gTyrLeuLys	LeuMetLysT	yrAsnSerTy	rAlaTrpMet	
GTGGTCCGAG	CAGAGATCCT	CAGGAACITT	CTCATCATTG	GAAGACTTAC	CAGAAACTTC	540
ValValArgA	laGluIlePh	eArgAsnPhe	LeuIleIleA	rgArgLeuTh	rArgAsnPhe	
CAAAACGAAT	TCGGGGGAGG	CGGATCCCGG	CTGGGGCTTT	GGGCGGGAGG	GGGCTCAGCG	600
GlnAsnGluP	heGlyGlyGl	yGlySerPro	LeuGlyLeuT	rpAlaGlyGl	yGlySerAla	
GCGGCACTAT	CCACCTGCAA	GACTATCGAC	ATGGAGCTGG	TGAAGCGGAA	GCGCATCGAG	660
AlaAlaLeuS	erThrCysLy	sThrIleAsp	MetGluLeuV	allLysArgLy	sArgIleGlu	
GCCATCCGCG	GCCAGATCCT	GTCCAAGCTG	CGGCTCGCCA	GCCCCCGGAG	CCAGGGGGAG	720
AlaIleArgG	lyGlnIleLe	uSerLysLeu	ArgLeuAlaS	erProProSe	rglnGlyGlu	
GTGCGCGCCG	GCGCGCTGCC	CGAGGCGGTG	CTCGCCCTGT	ACAACAGCAC	CGCGGACCGG	780
ValProProG	lyProLeuPr	oGluAlaVal	LeuAlaLeuT	yrAsnSerTh	rArgAspArg	
GTGGCGGGGG	AGAGTGCAGA	ACCGGAGCCC	GAGCCTGAGG	CGGACTACTA	CGCCAGGGAG	840
ValAlaGlyG	luSerAlaGl	uProGluPro	GluProGluA	laAspTyrTy	rAlaLysGlu	
GTCAACCGCG	TGCTAATGGT	GGAAACCCAC	AACGAAATCT	ATGACAAGTT	CAAGCAGAGT	900
ValThrArgV	alLeuMetVa	lGluThrHis	AsnGluIleT	yrAspLysPh	eLysGlnSer	
ACACACAGCA	TATATATGTT	CTTCAACACA	TCAGAGCTOC	GAGAAGCGGT	ACCTGAACCC	960
ThrHisSerI	leTyrMetPh	ePheAsnThr	SerGluLeuA	rgGluAlaVa	lProGluPro	

Fig. 2

[illegible]

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GTGTGCTCT	CCCGGGCAGA	GCTGGTCTTG	CTGAGGAGGC	TCAAGTTAAA	AGTGGAGCAG	1020
ValLeuLeuS	erArgAlaGl	uLeuArgLeu	LeuArgArgL	euLysLeuIy	sValGluGln	
CACGTGGAGC	TGTACCAGAA	ATACAGCAAC	AATTCTCTGGC	GATACCTCAG	CAACCGGCTG	1080
HisValGluL	euIyrGlnIy	sIyrSerAsn	AsnSerTrpA	rgIyrLeuSe	rAsnArgLeu	
CTGGCAACCA	GCGACTGGCC	AGAGTGGTTA	TCCTTTGATG	TCACCGGAGT	TGTGGCGCAG	1140
LeuAlaProS	erAspSerPr	cGluTrpLeu	SerPheAspV	alThrGlyVa	lValArgGln	
TGGTTGAGCC	GTGGAGGGGA	AATTGAGGGC	TTTCGCCCTTA	GCGCCCACTG	CTCTGTGAC	1200
TrpLeuSerA	rgGlyGlyGl	uIleGluGly	PheArgLeuS	erAlaHisCy	sSerCysAsp	
AGCAGGGATA	ACACACTTCA	AGTGGACATC	AACGGGTTC	CTACCGGCGG	CCGAGGTGAC	1260
SerArgAspA	snThrLeuGl	nValAspIle	AsnGlyPheT	hrThrGlyAr	gArgGlyAsp	
CTGGCCACCA	TTTATGGCAT	GAACCGGCTT	TTCTGCTTC	TCATGGCCAC	CCCGCTGGAG	1320
LeuAlaThrI	leHisGlyMe	tAsnArgPro	PheLeuLeuL	euMetAlaTh	rProLeuGlu	
AGGGCCACGC	ATCTGCAAAG	CtgaTCTAGA	CC			1352
ArgAlaGlnH	isLeuGlnSe	r...SerArg				

[illegible]

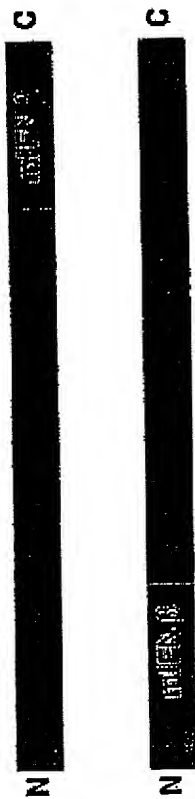
Fig. 3

Protein	Sequence	Reference
MMP-1/MMP-8		
Human type I collagen ($\alpha 1$)	Ala-Pro-Gln-Gly ₇₇₃ ~ Ile ₇₇₆ -Ala-Gly-Gln	80
Human type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₃ ~ Leu ₇₇₆ -Leu-Gly-Ala	80
Human type II collagen	Gly-Pro-Gln-Gly ₇₇₃ ~ Leu ₇₇₆ -Ala-Gly-Gln	80
Human type III collagen	Gly-Pro-Leu-Gly ₇₇₃ ~ Ile ₇₇₆ -Ala-Gly-Ile	80
Human α_2 -macroglobulin	Gly-Pro-Gln-Gly ₇₇₃ ~ Leu ₇₇₆ -Arg-Val-Gly	84
Rat α_2 -macroglobulin	Ala-Ala-Tyr-His ₆₈₁ ~ Leu ₆₈₄ -Val-Ser-Gln	84
Rat α_2 -macroglobulin	Met-Asp-Ala-Phe ₆₉₁ ~ Leu ₆₉₄ -Gln-Ser-Ser	84
Rat α_1 -macroglobulin	Glu-Pro-Gln-Ala ₆₈₃ ~ Leu ₆₈₆ -Ala-Met-Ser	84
Rat α_1 -macroglobulin	Gln-Ala-Leu-Ala ₆₈₅ ~ Met ₆₈₈ -Ser-Ala-Ile	84
Chicken ovostatin	Pro-Ser-Tyr-Phe ₆₇₃ ~ Leu ₆₇₆ -Asn-Ala-Gly	79
Human pregnancy zone protein	Tyr-Glu-Ala-Gly ₆₈₅ ~ Leu ₆₈₈ -Gly-Val-Val	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₆₈₇ ~ Val ₆₉₀ -Val-Glu-Arg	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₇₅₇ ~ Ile ₇₅₈ -Ser-Ser-Thr	84
α_1 -Protease inhibitor	Gly-Ala-Met-Phe ₅₅₂ ~ Leu ₅₅₃ -Glu-Ala-Ile	85
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~ Phe ₃₄₂ -Phe-Gly-Val	86
Human aggrecan	Thr-Glu-Gly-Glu ₇₇₃ ~ Ala ₇₇₆ -Arg-Gly-Ser	86
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~ Ile ₁₇ -Gln-Ala-Glu	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₀ ~ Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-2		
Guinea pig $\alpha 1$ (I) gelatin	Gly-Ala-Hyp-Gly ₃₄₇ ~ Leu ₃₅₀ -Glx-Gly-His	24
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Gln-Gly ₁₀₀ ~ Val ₁₀₁ -Arg-Gly-Glu	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₂₇₇ ~ Val ₂₇₈ -Gln-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ser-Gly ₃₀₁ ~ Leu ₃₀₂ -Hyp-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₃₃₁ ~ Glu ₃₃₂ -Arg-Gly-Ser	30
Rat $\alpha 1$ (I) gelatin	Gly-Ala-Lys-Gly ₃₅₁ ~ Leu ₃₅₂ -Thr-Gly-Ser	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₃₈₂ ~ Gln ₃₈₃ -Asp-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₆₃₄ ~ Phe ₆₃₅ -Ala-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ile-Gly ₆₇₆ ~ Asn ₆₇₇ -Val-Gly-Ala	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Hyl-Gly ₆₈₃ ~ Ser ₆₈₆ -Arg-Gly-Ala	30
Bovine type I collagen ($\alpha 1$)	Gly-Pro-Gln-Gly ₇₇₃ ~ Ile ₇₇₆ -Ala-Gly-Gln	22
Bovine type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₃ ~ Leu ₇₇₆ -Leu-Gly-Ala	22
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~ Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₆₂ ~ Tyr ₆₃ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~ Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~ Leu ₂₆ -Val-Glu-Ala	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₀ ~ Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-3		
Human α_2 -macroglobulin	Gly-Pro-Glu-Gly ₆₇₄ ~ Leu ₆₈₀ -Arg-Val-Gly	79
Human α_2 -macroglobulin	Arg-Val-Gly-Phe ₆₈₄ ~ Tyr ₆₈₅ -Glu-Ser-Asp	79
Human α_1 -antichymotrypsin	Leu-Leu-Ser-Ala ₃₆₀ ~ Leu ₃₆₁ -Val-Glu-Thr	91
α_1 -protease inhibitor	Glu-Ala-Ile-Pro ₃₃₇ ~ Met ₃₃₈ -Ser-Ile-Pro	91
Antithrombin III	Ile-Ala-Gly-Arg ₃₂₅ ~ Ser ₃₂₆ -Leu-Asn-Pro	91
Chicken ovostatin	Leu-Asn-Ala-Gly ₆₇₇ ~ Phe ₆₇₈ -Thr-Ala-Ser	79, 92
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~ Phe ₃₄₂ -Phe-Gly-Val	93
Substance P	Lys-Pro-Gln-Gln ₄ ~ Phe ₇ -Phe-Gly-Leu	37
Human ProMMP-1	Asp-Val-Ala-Gln ₅₈ ~ Phe ₆₁ -Val-Leu-Thr	43
Human ProMMP-3	Asp-Thr-Leu-Glu ₆₁ ~ Val ₆₉ -Met-Arg-Lys	94
Human ProMMP-3	Asp-Val-Gly-His ₈₂ ~ Phe ₈₃ -Arg-Thr-Phe	94
Human ProMMP-8	Asp-Ser-Gly-Gly ₇₄ ~ Phe ₇₇ -Met-Leu-Thr	95
Human ProMMP-9	Arg-Val-Ala-Glu ₄₀ ~ Met ₄₁ -Arg-Gly-Glu	48
Human ProMMP-9	Asp-Leu-Gly-Arg ₆₇ ~ Phe ₇₀ -Gln-Thr-Phe	48
Human fibronectin	Pro-Phe-Ser-Pro ₆₄₈ ~ Leu ₆₆₀ -Val-Ala-Thr	21

Fig. 4

	Sequence	Reference
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₆ ~Leu ₁₀₀ -Leu-Pro-Ala	88
	Ala-Pro-Gly-Asn ₁₀₀ ~Ala ₁₁₀ -Ser-Glu-Ser	88
	Phe-Ser-Ser-Glu ₁₁₆ ~Ser ₁₁₇ -Lys-Arg-Glu	88
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Ala-Gly-Gly-Ala ₁₁₃ ~Gln ₁₁₄ -Met-Gly-Val	96
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Gln-Met-Gly-Val ₁₁₉ ~Met ₁₂₀ -Gln-Gly-Pro	96
Bovine $\alpha 1$ (IX) collagen, NC2	Met-Ala-Ala-Ser~Leu-Lys-Arg-Pro	96
Bovine $\alpha 2$ (IX) collagen, NC2	~Ala-Lys-Arg-Glu	96
Bovine $\alpha 3$ (IX) collagen, NC2	~Leu-Arg-Lys-Pro	96
Bovine $\alpha 1$ (XI) collagen, N-telopeptide	Gln-Ala-Gln-Ala~As-Leu-Gln-Gln	96
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Bovine insulin, B chain	Leu-Val-Glu-Ala ₁₄ ~Leu ₁₅ -Tyr-Leu-Val	97
Bovine insulin, B chain	Glu-Ala-Leu-Tyr ₁₅ ~Leu ₁₇ -Val-Cys-Gly	21, 97
MMP-7		
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87
Human prourokinase	Pro-Pro-Glu-Glu ₁₄₃ ~Leu ₁₄₄ -Lys-Phe-Gln	98
MMP-9		
Human type V collagen ($\alpha 1$)	Gly-Pro-Pro-Gly ₄₃₉ ~Val ₄₄₀ -Val-Gly-Pro	99
Human type V collagen ($\alpha 2$)	Gly-Pro-Pro-Gly ₄₄₅ ~Leu ₄₄₆ -Arg-Gly-Glu	99
Human type XI collagen ($\alpha 1$)	Gly-Pro-Gly-Gly ₄₃₉ ~Val ₄₄₀ -Val-Gly-Pro	99
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₆₂ ~Tyr ₆₃ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
MMP-10		
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87

A.



B.

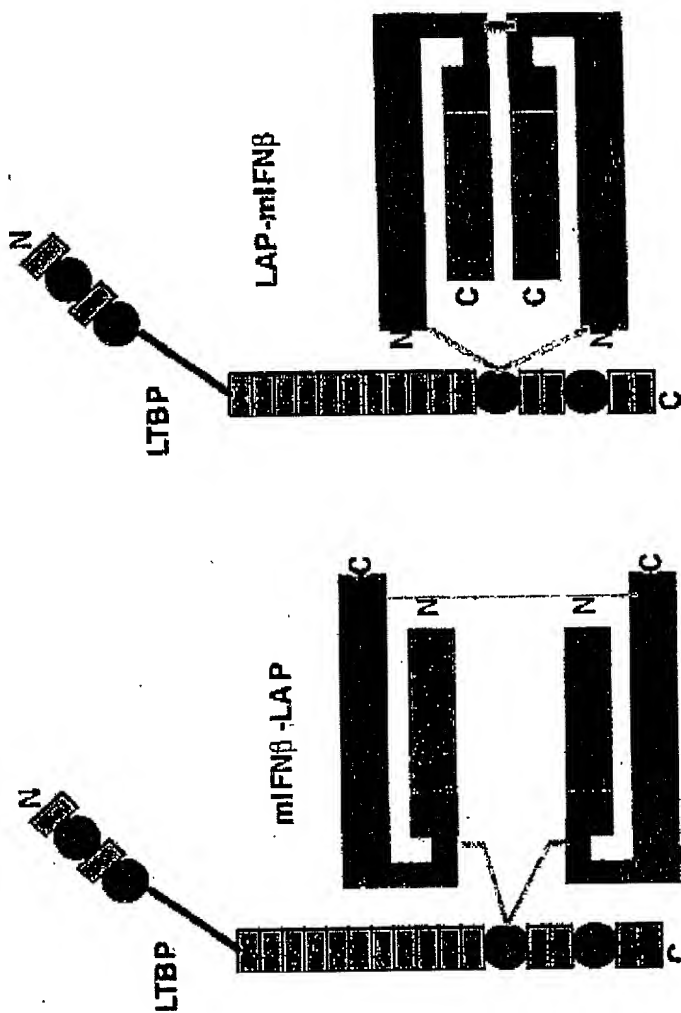


Fig. 5

TABLE 1

M.W. 1 2 3

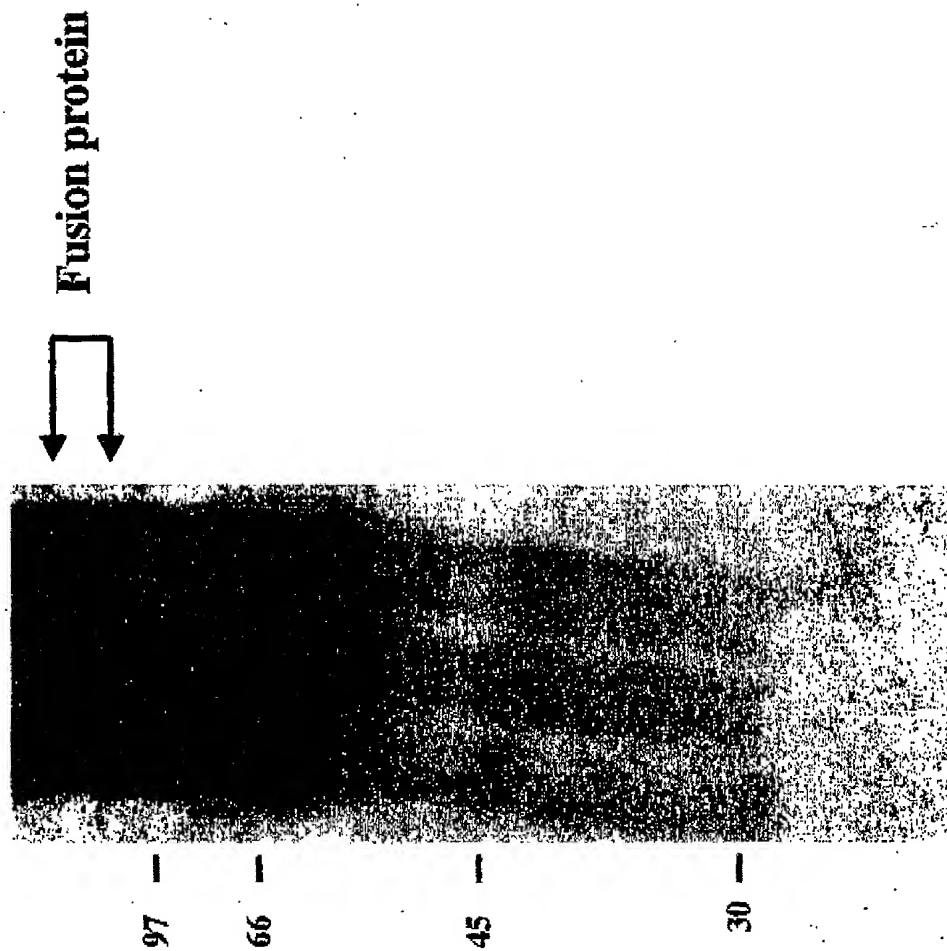


Fig. 6

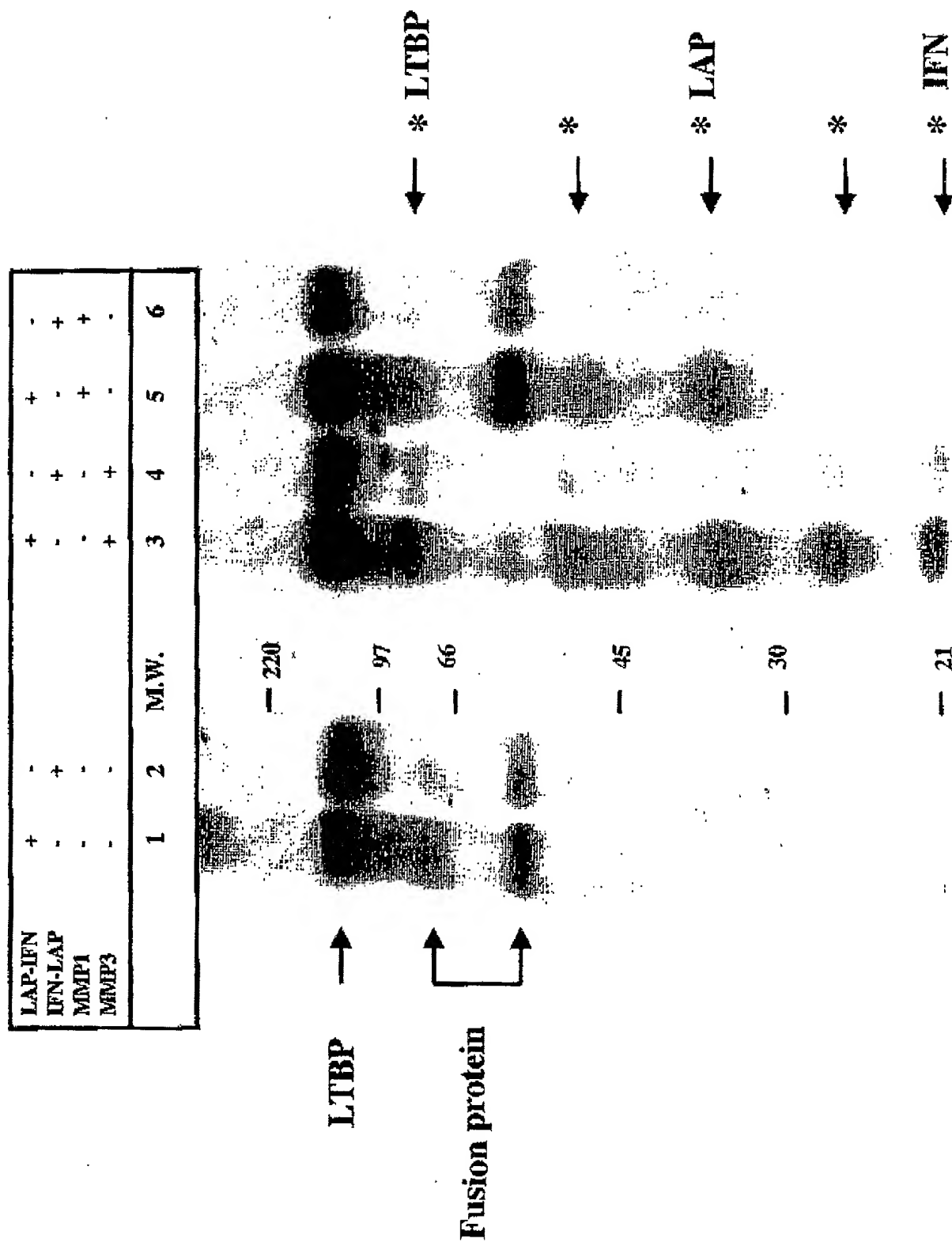


Fig. 7

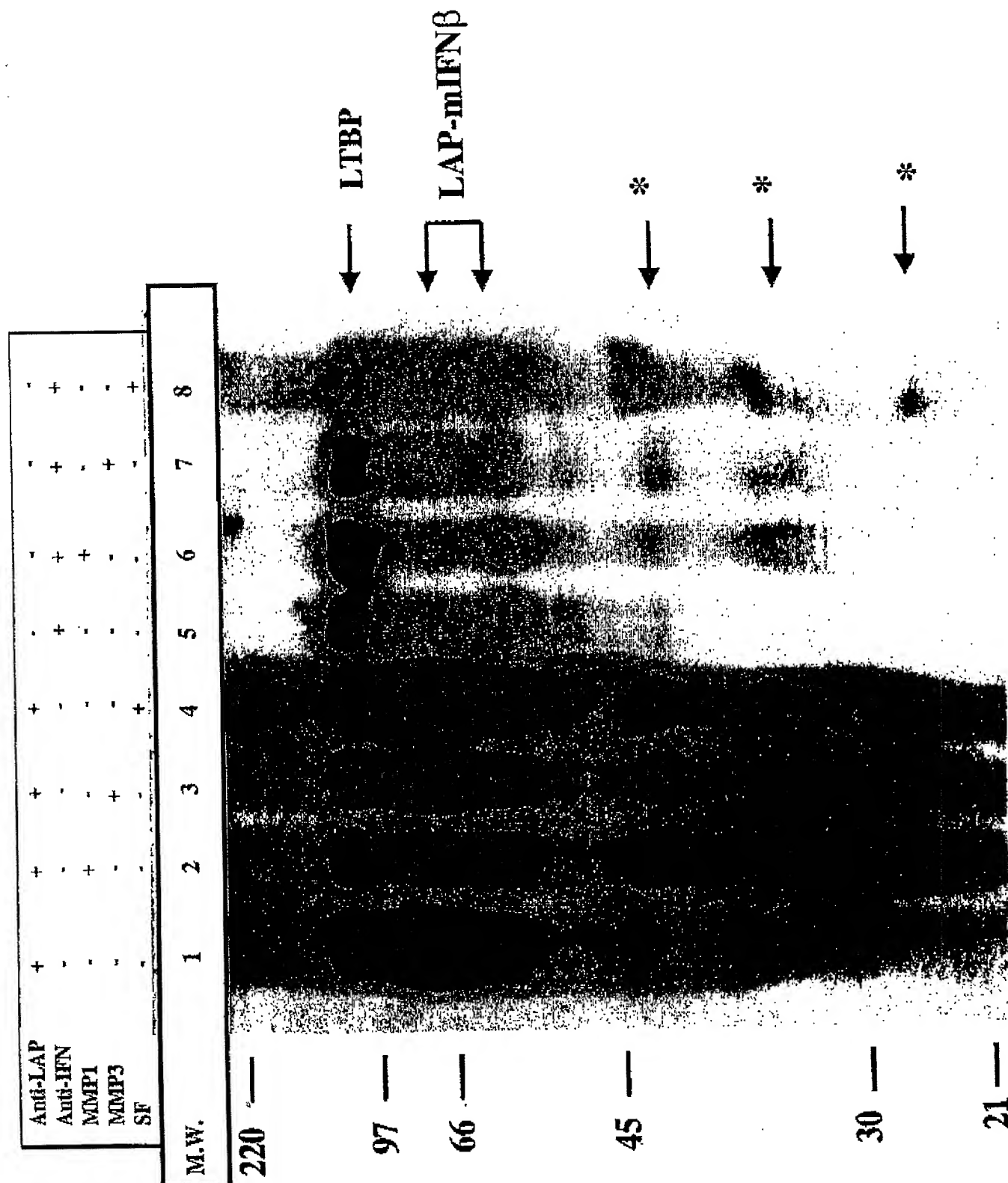


Fig. 8a

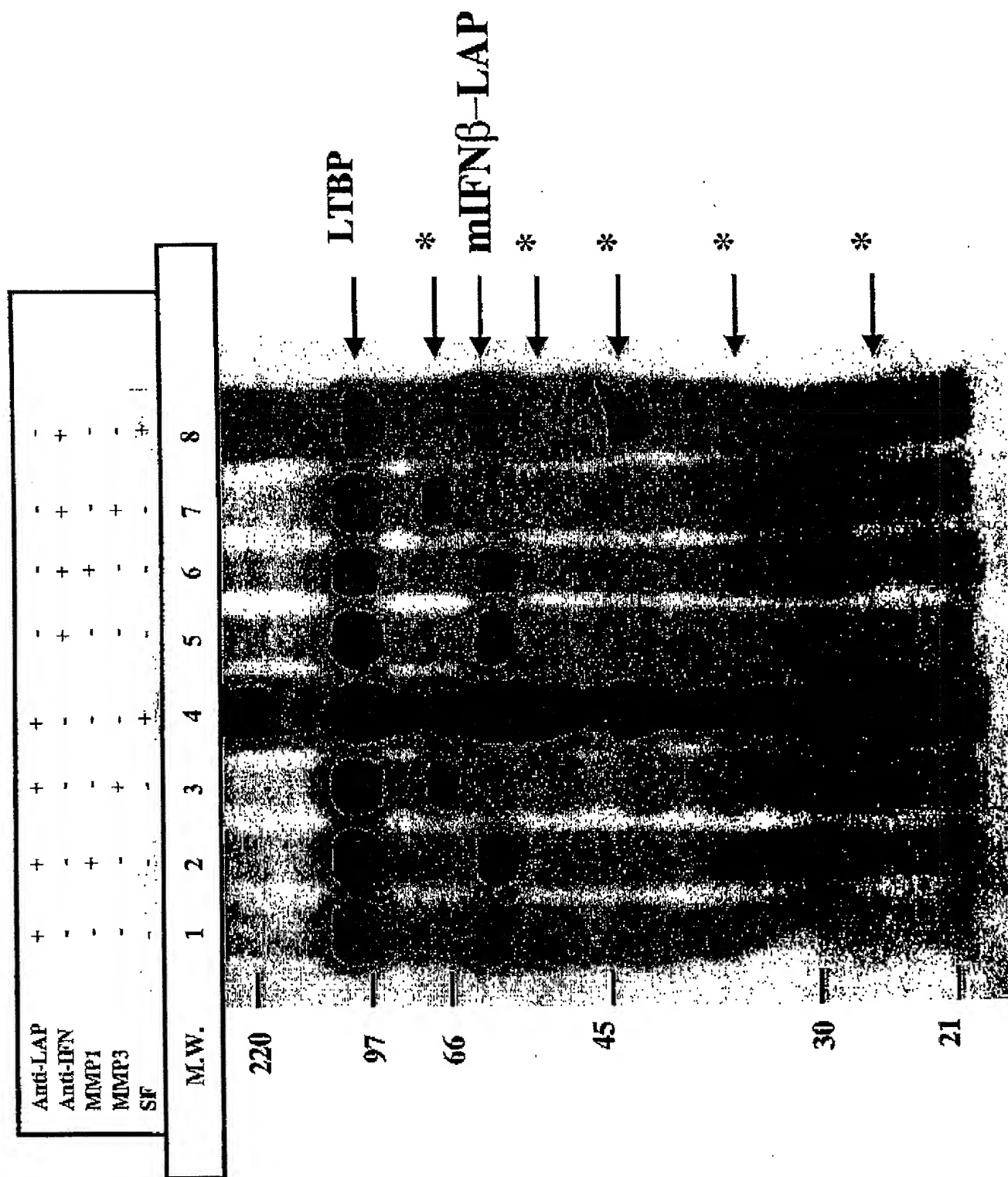
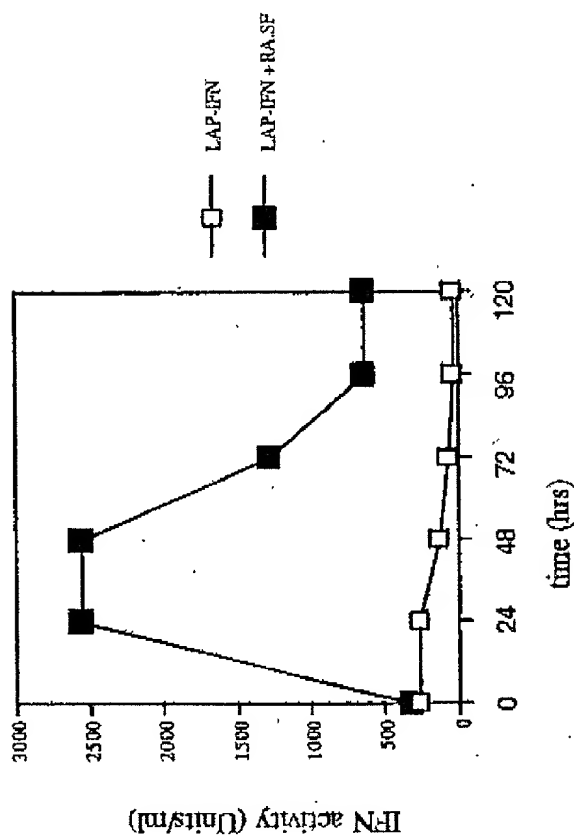


Fig. 8b

A.



B.

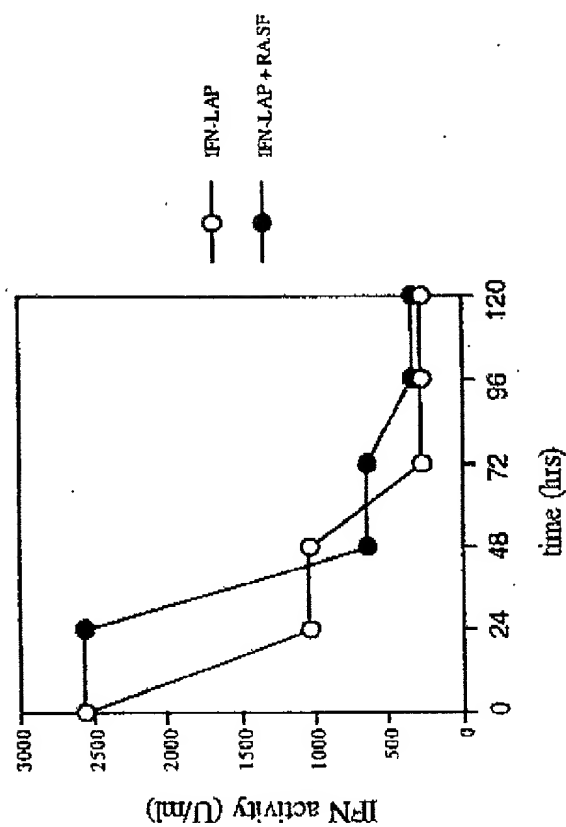
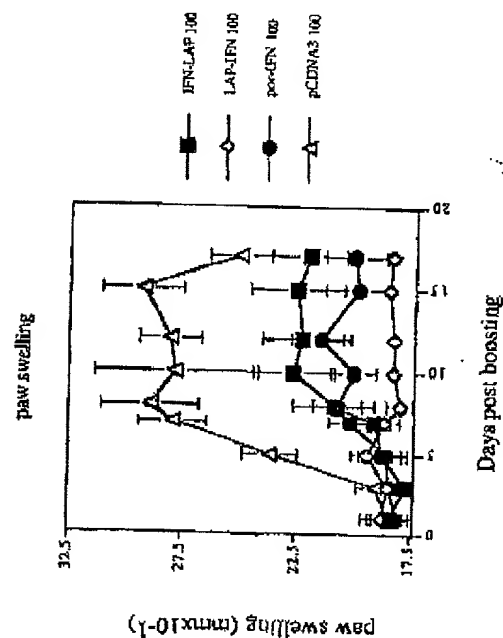


Fig. 9

A.



B.

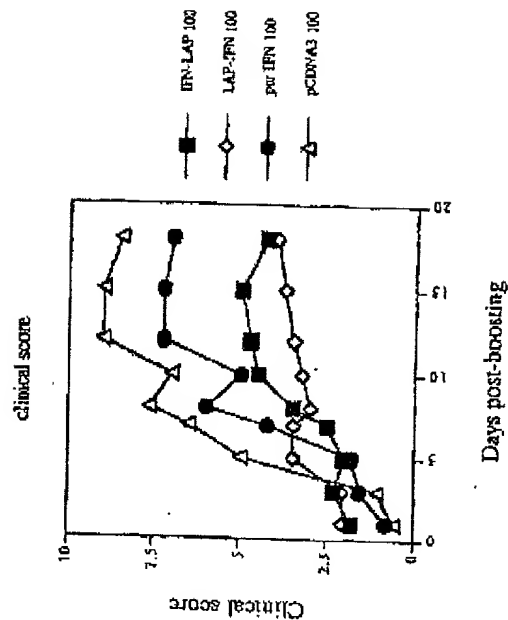


Fig. 10